OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/017,066

DATE: 04/26/2002
TIME: 14:29:50

Input Set : N:\Crf3\RULE60\10017066.raw
Output Set: N:\CRF3\04262002\J017066.raw

ENTERED

<110> APPLICANT: Arthur B. Raitano
Daniel E.H. Afar
Aya Jakobovits
Mary Faris
Rene S. Hubert
Steve Chappell Mitchell
Douglas C. Saffran
<120> TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR
UP-REGULATED IN PROSTATE CANCER AND USES THEREOF
<130> FILE REFERENCE: 129.24USU1
<140> CURRENT APPLICATION NUMBER: 10/017,066
<141> CURRENT FILING DATE: 2001-12-14
<150> PRIOR APPLICATION NUMBER: US/09/680,728
<151> PRIOR FILING DATE: 2000-10-05
<160> NUMBER OF SEQ ID NOS: 50
<170> SOFTWARE: FastSEQ for Windows Version 4.0
<210> SEQ ID NO: 1
<211> LENGTH: 3136
<212> TYPE: DNA
<213> ORGANISM: Homo Sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (133)...(1083)
<400> SEQUENCE: 1

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ggggtcacac attccttcca tacggttgag cctctacctg cctggtgctg gtcacagttc     120
agcttcttca tg atg gtg gat ccc aat ggc aat gaa tcc agt gct aca tac      171
                Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr
                 1               5                  10
ttc atc cta ata ggc ctc cct ggt tta gaa gag gct cag ttc tgg ttg      219
Phe Ile Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu
     15                  20                  25
gcc ttc cca ttg tgc tcc ctc tac ctt att gct gtg cta ggt aac ttg      267
Ala Phe Pro Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu
 30                  35                  40                  45
aca atc atc tac att gtg cgg act gag cac agc ctg cat gag ccc atg      315
Thr Ile Ile Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met
                 50                  55                  60
tat ata ttt ctt tgc atg ctt tca ggc att gac atc ctc atc tcc acc      363
Tyr Ile Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr
             65                  70                  75
tca tcc atg ccc aaa atg ctg gcc atc ttc tgg ttc aat tcc act acc      411
Ser Ser Met Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr
```

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Input Set : N:\Crf3\RULE60\10017066.raw
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```
45                80                  85                  90
46      atc cag ttt gat gct tgt ctg cta cag att ttt gcc atc cac tcc tta      459
47      Ile Gln Phe Asp Ala Cys Leu Leu Gln Ile Phe Ala Ile His Ser Leu
48           95                  100                 105
49      tct ggc atg gaa tcc aca gtg ctg ctg gcc atg gct ttt gac cgc tat      507
50      Ser Gly Met Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr
51      110                 115                 120                 125
52      gtg gcc atc tgt cac cca ctg cgc cat gcc aca gta ctt acg ttg cct      555
53      Val Ala Ile Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro
54                      130                 135                 140
55      cgt gtc acc aaa att ggt gtg gct gct gtg gtg cgg ggg gct gca ctg      603
56      Arg Val Thr Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu
57                  145                 150                 155
58      atg gca ccc ctt cct gtc ttc atc aag cag ctg ccc ttc tgc cgc tcc      651
59      Met Ala Pro Leu Pro Val Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser
60              160                 165                 170
61      aat atc ctt tcc cat tcc tac tgc cta cac caa gat gtc atg aag ctg      699
62      Asn Ile Leu Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu
63          175                 180                 185
64      gcc tgt gat gat atc cgg gtc aat gtc gtc tat ggc ctt atc gtc atc      747
65      Ala Cys Asp Asp Ile Arg Val Asn Val Val Tyr Gly Leu Ile Val Ile
66      190                 195                 200                 205
67      atc tcc gcc att ggc ctg gac tca ctt ctc atc tcc ttc tca tat ctg      795
68      Ile Ser Ala Ile Gly Leu Asp Ser Leu Leu Ile Ser Phe Ser Tyr Leu
69                      210                 215                 220
70      ctt att ctt aag act gtg ttg ggc ttg aca cgt gaa gcc cag gcc aag      843
71      Leu Ile Leu Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys
72                  225                 230                 235
73      gca ttt ggc act tgc gtc tct cat gtg tgt gct gtg ttc ata ttc tat      891
74      Ala Phe Gly Thr Cys Val Ser His Val Cys Ala Val Phe Ile Phe Tyr
75              240                 245                 250
76      gta cct ttc att gga ttg tcc atg gtg cat cgc ttt agc aag cgg cgt      939
77      Val Pro Phe Ile Gly Leu Ser Met Val His Arg Phe Ser Lys Arg Arg
78          255                 260                 265
79      gac tct ccg ctg ccc gtc atc ttg gcc aat atc tat ctg ctg gtt cct      987
80      Asp Ser Pro Leu Pro Val Ile Leu Ala Asn Ile Tyr Leu Leu Val Pro
81      270                 275                 280                 285
82      cct gtg ctc aac cca att gtc tat gga gtg aag aca aag gag att cga     1035
83      Pro Val Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Glu Ile Arg
84                      290                 295                 300
85      cag cgc atc ctt cga ctt ttc cat gtg gcc aca cac gct tca gag ccc     1083
86      Gln Arg Ile Leu Arg Leu Phe His Val Ala Thr His Ala Ser Glu Pro
87                  305                 310                 315
88      taggtgtcag tgatcaaact tcttttccat tcagagtcct ctgattcaga ttttaatgtt   1143
89      aacattttgg aagacagtat tcagaaaaaa aatttcctta ataaaaaata caactcagat   1203
90      ccttcaaata tgaaactggt tggggaatct ccatttttc aatattattt tcttctttgt   1263
91      tttcttgcta catataatta ttaataccct gactaggttg tggttggagg gttattactt   1323
92      ttcattttac catgcagtcc aaatctaaac tgcttctact gatggtttac agcattctga   1383
93      gataagaatg gtacatctag agaacatttg ccaaaggcct aagcacggca aaggaaaata   1443
```

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Input Set : N:\Crf3\RULE60\10017066.raw
Output Set: N:\CRF3\04262002\J017066.raw

aacacagaat ataataaaat gagataatct agcttaaaac tataacttcc tcttcagaac 1503
tcccaaccac attggatctc agaaaaatgc tgtcttcaaa atgacttcta cagagaagaa 1563
ataatttttc ctctggacac tagcacttaa ggggaagatt ggaagtaaag ccttgaaaag 1623
agtacattta cctacgttaa tgaaagttga cacactgttc tgagagtttt cacagcatat 1683
ggaccctgtt tttcctattt aattttctta tcaacccttt aattaggcaa agatattatt 1743
agtaccctca ttgtagccat gggaaaattg atgttcagtg gggatcagtg aattaaatgg 1803
ggtcatacaa gtataaaaat taaaaaaaaa aaagacttca tgcccaatct catatgatgt 1863
ggaagaactg ttagagagac caacagggta gtgggttaga gatttccaga gtcttacatt 1923
ttctagagga ggtatttaat ttcttctcac tcatccagtg ttgtatttag gaatttcctg 1983
gcaacagaac tcatggcttt aatcccacta gctattgctt attgtcctgg tccaattgcc 2043
aattacctgt gtcttggaag aagtgatttc taggttcacc attatggaag attcttattc 2103
agaaagtctg catagggctt atagcaagtt atttattttt aaaagttcca taggtgattc 2163
tgataggcag tgaggttagg gagccaccag ttatgatggg aagtatggaa tggcaggtct 2223
tgaagataac attggccttt tgagtgtgac tcgtagctgg aaagtgaggg aatcttcagg 2283
accatgcttt atttggggct ttgtgcagta tggaacaggg actttgagac caggaaagca 2343
atctgactta ggcatgggaa tcaggcattt ttgcttctga ggggctatta ccaagggtta 2403
ataggtttca tcttcaacag gatatgacaa cagtgttaac caagaaactc aaattacaaa 2463
tactaaaaca tgtgatcata tatgtggtaa gtttcatttt ctttttcaat cctcaggttc 2523
cctgatatgg attcctataa catgctttca tccccttttg taatggatat catatttgga 2583
aatgcctatt taatacttgt atttgctgct ggactgtaag cccatgaggg cactgtttat 2643
tattgaatgt catctctgtt catcattgac tgctctttgc tcatcattga atcccccagc 2703
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ttccttctgt cctgaacaca tagccaggca attttccagc cttctttgag ttgggtatta 2823
ttaaattctg gccattactt ccaatgtgag tggaagtgac atgtgcaatt tctatacctg 2883
gctcataaaa ccctcccatg tgcagccttt catgttgaca ttaaatgtga cttgggaagc 2943
tatgtgttac acagagtaaa tcaccagaag cctggatttc tgaaaaaact gtgcagagcc 3003
aaacctctgt catttgcaac tcccacttgt atttgtacga ggcagttgga taagtgaaaa 3063
ataaagtact attgtgtcaa gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3123
aaaaaaaaaa aaa 3136

<210> SEQ ID NO: 2
<211> LENGTH: 317
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens
<400> SEQUENCE: 2

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1 5 10 15
Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu Ala Phe Pro
20 25 30
Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu Thr Ile Ile
35 40 45
Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile Phe
50 55 60
Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr Ser Ser Met
65 70 75 80
Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln Phe
85 90 95
Asp Ala Cys Leu Leu Gln Ile Phe Ala Ile His Ser Leu Ser Gly Met
100 105 110
Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile

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```
144                 115                 120                 125
145       Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val Thr
146           130                 135                 140
147       Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu Met Ala Pro
148       145                 150                 155                 160
149       Leu Pro Val Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile Leu
150                       165                 170                 175
151       Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Asp
152                   180                 185                 190
153       Asp Ile Arg Val Asn Val Val Tyr Gly Leu Ile Val Ile Ile Ser Ala
154               195                 200                 205
155       Ile Gly Leu Asp Ser Leu Leu Ile Ser Phe Ser Tyr Leu Leu Ile Leu
156           210                 215                 220
157       Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys Ala Phe Gly
158       225                 230                 235                 240
159       Thr Cys Val Ser His Val Cys Ala Val Phe Ile Phe Tyr Val Pro Phe
160                       245                 250                 255
161       Ile Gly Leu Ser Met Val His Arg Phe Ser Lys Arg Arg Asp Ser Pro
162                   260                 265                 270
163       Leu Pro Val Ile Leu Ala Asn Ile Tyr Leu Leu Val Pro Pro Val Leu
164               275                 280                 285
165       Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Glu Ile Arg Gln Arg Ile
166           290                 295                 300
167       Leu Arg Leu Phe His Val Ala Thr His Ala Ser Glu Pro
168       305                 310                 315
170 <210> SEQ ID NO: 3
171 <211> LENGTH: 320
172 <212> TYPE: PRT
173 <213> ORGANISM: Rat Protein
174 <400> SEQUENCE: 3
175       Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Met Leu Ile Gly Ile
176        1               5                  10                  15
177       Pro Gly Leu Glu Glu Ala His Phe Trp Phe Gly Phe Pro Leu Leu Ser
178                   20                  25                  30
179       Met Tyr Ala Val Ala Leu Phe Gly Asn Cys Ile Val Val Phe Ile Val
180               35                  40                  45
181       Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
182           50                  55                  60
183       Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile
184       65                  70                  75                  80
185       Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Thr Phe Asp Ala Cys
186                       85                  90                  95
187       Leu Ala Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr
188                   100                 105                 110
189       Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
190               115                 120                 125
191       Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Val Gln Ile Gly
192           130                 135                 140
193       Met Val Ala Leu Val Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu
```

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Input Set : N:\Crf3\RULE60\10017066.raw
Output Set: N:\CRF3\04262002\J017066.raw

```
194       145                 150                 155                 160
195       Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser
196                       165                 170                 175
197       Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Thr Asp Thr Leu
198                   180                 185                 190
199       Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val
200               195                 200                 205
201       Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Ala Val
202           210                 215                 220
203       Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys
204       225                 230                 235                 240
205       Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly
206                       245                 250                 255
207       Leu Ser Val Val His Arg Phe Gly Asn Ser Leu Asp Pro Ile Val His
208                   260                 265                 270
209       Val Leu Met Gly Asp Val Tyr Leu Leu Leu Pro Pro Val Ile Asn Pro
210               275                 280                 285
211       Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala
212           290                 295                 300
213       Met Phe Lys Ile Ser Cys Asp Lys Asp Ile Glu Ala Gly Gly Asn Thr
214       305                 310                 315                 320
216 <210> SEQ ID NO: 4
217 <211> LENGTH: 320
218 <212> TYPE: PRT
219 <213> ORGANISM: Homo Sapiens
220 <400> SEQUENCE: 4
221       Met Ser Ser Cys Asn Phe Thr His Ala Thr Cys Val Leu Ile Gly Ile
222        1               5                  10                  15
223       Pro Gly Leu Glu Lys Ala His Phe Trp Val Gly Phe Pro Leu Leu Ser
224                   20                  25                  30
225       Met Tyr Val Val Ala Met Cys Gly Asn Cys Ile Val Val Phe Ile Val
226               35                  40                  45
227       Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
228           50                  55                  60
229       Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile
230       65                  70                  75                  80
231       Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Ser Ile Glu Ala Cys
232                       85                  90                  95
233       Leu Thr Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr
234                   100                 105                 110
235       Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
236               115                 120                 125
237       Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Ala Gln Ile Gly
238           130                 135                 140
239       Ile Val Ala Val Val Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu
240       145                 150                 155                 160
241       Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser
242                       165                 170                 175
243       Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Ala Asp Thr Leu
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 04/26/2002
PATENT APPLICATION: US/10/017,066 TIME: 14:29:51

Input Set : N:\Crf3\RULE60\10017066.raw
Output Set: N:\CRF3\04262002\J017066.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:41; N Pos. 6,12,15
Seq#:42; N Pos. 3,6,12,15
Seq#:43; N Pos. 12,15
Seq#:44; N Pos. 3,12,15
Seq#:45; N Pos. 3,9,18
Seq#:46; N Pos. 3,9
Seq#:47; N Pos. 6,9,21
Seq#:48; N Pos. 1,13,16
Seq#:49; N Pos. 1,7,10,16
Seq#:50; N Pos. 10,16,19

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/017,066

DATE: 04/26/2002
TIME: 14:29:51

Input Set : N:\Crf3\RULE60\10017066.raw
Output Set: N:\CRF3\04262002\J017066.raw

L:630 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:633 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:41
L:634 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:0
L:642 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:645 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:42
L:646 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:0
L:654 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:657 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:43
L:658 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:0
L:666 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:669 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:44
L:670 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:0
L:678 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:681 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:45
L:682 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:0
L:690 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:693 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:46
L:694 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46 after pos.:0
L:702 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:705 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:47
L:706 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47 after pos.:0
L:714 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:717 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:48
L:718 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48 after pos.:0
L:726 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:729 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:49
L:730 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49 after pos.:0
L:738 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:741 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:50
L:742 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50 after pos.:0